

What is claimed is:

1. A method for modeling cellular metabolism of an organism, comprising:
constructing a flux balance analysis model;
applying constraints to the flux balance analysis model, the constraints selected from the set consisting of: qualitative kinetic information constraints, qualitative regulatory information constraints, and differential DNA microarray experimental data constraints.
2. The method of claim 1 wherein the constraints are logic constraints selected to protect against violation of a kinetic or regulatory barrier.
3. The method of claim 1 wherein the constraints are connectivity restraints.
4. The method of claim 1 further comprising the step of applying mixed-integer linear programming to solve for a desired metabolic outcome.
5. The method of claim 1 further comprising the step of solving for a desired metabolic outcome.
6. A method for modeling cellular metabolism of an organism that improves upon a flux balance analysis model, comprising:
constructing the flux balance analysis model; and
applying a plurality of logic constraints to the flux balance analysis model.

7. The method of claim 6, further comprising selecting the set of logic constraints to protect against violation a kinetic or regulatory barrier.
8. The method of claim 6 wherein the logic constraints are defined by a relationship between changes in reaction fluxes and metabolic concentrations.
9. The method of claim 6 wherein the logic constraints are defined by a relationship between reaction fluxes and transcript levels of gene coding.
10. The method of claim 6 wherein the logic constraints are represented by binary variables.
11. The method of claim 10 wherein a first binary variable represents the presence of a reaction and a second binary variable represents the absence of a reaction.
12. The method of claim 6 further comprising applying a computational procedure to identify a minimal set of metabolic reactions.
13. The method of claim 12 further comprising selecting a growth rate, and wherein the step of applying a computational procedure is applying a computational procedure to identify the minimal set of metabolic reactions capable of supporting the growth rate.
14. The method of claim 6 further comprising the step of applying mixed-integer linear programming to solve for a desired metabolic outcome.

15. The method of claim 6 further comprising the step of solving for a desired metabolic outcome.

16. The method of claim 15 further comprising engineering a change in an organism based on the desired metabolic outcome.

17. A method for determining a reduced genome, comprising:
selecting a minimal set of reactions from a set of metabolic reactions that meets a growth rate target;
mapping enzymes catalyzing the minimal set of reactions to a corresponding set of coding genes, the corresponding set of coding genes defining a reduced genome.

18. The method of claim 16 wherein the growth rate target is a biomass target production rate.

19. A system for modeling cellular metabolism of an organism, comprising:
a flux balance analysis model;
a plurality of constraints applied to the flux balance analysis model, the constraints selected from the set consisting of: qualitative kinetic information constraints, qualitative regulatory information constraints, and differential DNA microarray experimental data constraints.